REMARKS

Claims 91-105 are now pending, with claim 91 being the sole independent claim.

Claims 27-90 have been canceled without prejudice to or disclaimer of the subject matter recited therein.

Claims 91-105 have been added. Support for the reference to "cyclin delta activity" in claim 91 is found at least in Example 10, the paragraph at page 30, lines 3-10 of the specification. Support for the sequence identities recited in claims 91-94 is found at least in the paragraph beginning on line 29 of page 6 and continuing onto page 7 of the specification. Support for the use of the term "recombinant" in claims 98, 100, and 102-105 is found at least in the paragraph beginning on line 37 of page 10 and continuing onto page 11 of the specification. Support for claims 101-103 are found at least in Examples 7-8, pages 24-28 of the specification. Support for claim 104 is found at least in the paragraph at page 2, lines 27-34 of the specification. Support for claim 105 is found at least in Examples 9-10, pages 28-30 of the specification. No new matter has been added.

The specification has been amended at two locations to remove reference to the following URL: www.ncbi.nlm.nih.gov/BLAST/.

RESPONSE TO RESTRICTION REQUIREMENT

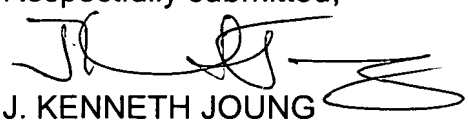
In response to the Restriction Requirement in the Office Action, Applicants hereby elect, without traverse, Group I (claims 27-32, 38-42, 43-48, 54-58, 59-64, 70-74, 75-80 and 86-90). Applicants also select SEQ ID No:11 and SEQ ID NO:12, for a single nucleotide sequence and its corresponding amino acid sequence, respectively.

Applicants submit that now pending claims 91-105 are directed to Group I.

Please charge any fees or credit any overpayment of fees which are required in connection herewith to Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company).

In view of the foregoing, allowance of the above-referenced application is respectfully requested.

Respectfully submitted,



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Dated: 7 October 2002

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In showing the changes, deleted material is shown within brackets, and inserted material is shown underlined.

IN THE SPECIFICATION:

Paragraph at page 7, lines 5-27:

A "substantial portion" of an amino acid or nucleotide sequence comprises enough of the amino acid sequence of a polypeptide or the nucleotide sequence of a gene to afford putative identification of that polypeptide or gene, either by manual evaluation of the sequence by one skilled in the art, or by computer-automated sequence comparison and identification using algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul, S. F., et al., (1993) *J. Mol. Biol. 215*:403-410[; see also www.ncbi.nlm.nih.gov/BLAST/]). In general, a sequence of ten or more contiguous amino acids or thirty or more nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene specific oligonucleotide probes comprising 20-30 contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12-15 bases may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises enough of the sequence to afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches partial or complete amino acid and nucleotide sequences encoding one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

Paragraph at page 18, lines 8-25:

ESTs encoding cyclin proteins were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., et al., (1993) *J. Mol. Biol. 215*:403-410[; see also www.ncbi.nlm.nih.gov/BLAST/]) searches for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS

translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish, W. and States, D. J. (1993) *Nature Genetics 3*:266-272 and Altschul, Stephen F., et al. (1997) *Nucleic Acids Res. 25*:3389-3402) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.